

SPLICE FORM 1:

```

1   CGTCCTTCCT GGTCTGCGG GTCCAGGACT GTCCGCGGGG TTGAGGGAAG
51  GGGCCGTGCC CGGTGCCAGC CCAGGTGCTC GCGGCCTGGC TCCATGGCCC
101 TGGTCACAGT GAGCCGTTCG CCCCCGGGCA GCGGCGCCTC CACGCCCCTG
151 GGGCCCTGGG ACCAGGCGGT CCAGCGAAGG AGTCGACTCC AGCGAAGGCA
201 GAGCTTTGCG GTGCTCCGTG GGGCTGTCCT GGGACTGCAG GATGGAGGGG
251 ACAATGATGA TGCAGCAGAG GCCAGTTCTG AGCCAACAGA GAAGGCCCCG
301 AGTGAGGAGG AGCTCCACGG GGACCAGACA GACTTCGGGC AAGGATCCCA
351 GAGTCCCCAG AAGCAGGAGG AGCAGAGGCA GCACCTGCAC CTCATGGTAC
401 AGCTGCTGAG GCCGAGGAT GACATCCGCC TGGCAGCCCA GCTGGAGGCA
451 CCCCCGGCTC CCGGCTCCG CTACCTGCTG GTAGTTTCTA CACGAGAAGG
501 AGAAGGTCTG AGCCAGGATG AGACGGTCCT CCTGGGCGTG GATTTCCCTG
551 ACAGCAGCTC CCCCAGCTGC ACCCTGGGCC TGGTCTTGCC CCTCTGGAGT
601 GACACCCAGG TGTACTTAGA TGGAGACGGG GGCTTCAGCG TGACGTCTGG
651 TGGGCAAAGC CGGATCTTCA AGCCCATCTC CATCCAGACC ATGTGGGCCA
701 CACTCCAGGT ATTGCACCAA GCATGTGAGG CAGCTCTAGG CAGCGGCCTT
751 GTACCGGGTG GCAGTGCCCT CACCTGGGCC AGCCACTACC AGGAGAGACT
801 GAACTCCGAA CAGAGCTGCC TCAATGAGTG GACGGCTATG GCCGACCTGG
851 AGTCTCTGCG GCCTCCAGC GCCGAGCCTG GCGGGTCCTC AGAACAGGAG
901 CAGATGGAGC AGGCGATCCG TGCTGAGCTG TGGAAAGTGT TGGATGTCAG
951 TGACCTGGAG AGTGTCACTT CCAAAGAGAT CCGCCAGGCT CTGGAGCTGC
1001 GCCTGGGGCT CCCCCTCCAG CAGTACCGTG ACTTCATCGA CAACCAGATG
1051 CTGCTGCTGG TGGCACAGCG GGACCGAGCC TCCCGCATCT TCCCCACCT
1101 CTACCTGGGC TCAGAGTGGA ACGCAGCAAA CCTGGAGGAG CTGCAGAGGA
1151 ACAGGGTCAC CCACATCTTG AACATGGCCC GGGAGATTGA CAACTTCTAC
1201 CCTGAGCGCT TCACCTACCA CAATGTGCGC CTCTGGGATG AGGAGTCGGC
1251 CCAGCTGCTG CCGCACTGGA AGGAGACGCA CCGCTTCATT GAGGCTGCAA
1301 GAGCACAGGG CACCCACGTG CTGGTCCACT GCAAGATGGG CGTCAGCCGC
1351 TCAGCGGCCA CAGTGTGCGC CTATGCCATG AAGCAGTACG AATGCAGCCT
1401 GGAGCAGGCC CTGCGCCACG TGCAGGAGCT CCGGCCCATC GCCCGCCCCA
1451 ACCCTGGCTT CCTGCGCCAG CTGCAGATCT ACCAGGGCAT CCTGACGGCC
1501 AGAACCTGAG GGTGGTGGGG AGGAGAAGGT TGTAGGCATG GAAGAGAGCC
1551 AGGCAGCCCC GAAAGAAGAG CCTGGGCCAC GGCCACGTAT AAACCTCCGA
1601 GGGGTCATGA GGTCCATCAG TCTTCTGGAG CCCTCCTTGG AGCTGGAGAG
1651 CACCTCAGAG ACCAGTGACA TGCCAGAGGT CTTCTCTTCC CACGAGTCTT
1701 CACATGAAGA GCCTCTGCAG CCCTTCCAC AGCTTGCAAG GACCAAGGGA
1751 GGCCAGCAGG TGGACAGGGG GCCTCAGCCT GCCCTGAAGT CCCGCCAGTC
1801 AGTGGTTACC CTCCAGGGCA GTGCCGTGGT GGCCAACCGG ACCCAGGCCT
1851 TCCAGGAGCA GGAGCAGGGG CAGGGGCAGG GGCAGGGAGA GCCCTGCATT
1901 TCCTCTACGC CCAGGTTCCG GAAGGTGGTG AGACAGGCCA GCGTGCATGA
1951 CAGTGGAGAG GAGGGCGAGG CCTGAGCCCT CACACATGCC CACGCTCCCC
2001 TGACACTGAA GAGGATCCAC AACTCCTTGG AGAAACACCC TCACGTCTGT
2051 TGCCGCACAC ATTCTCTCA GCTCCGCCCC ATACCCGTCA CTACAGCCTC
2101 ACCTCCCACC CCTGTCACTA CGGCCTCACC TCCCACCCCT GTCACACAG
2151 CCTCACCTCC TACAGCCTTA AGTCCCAGGC CCATGTCTGC CTGTCCAAGG
2201 GCTCAAGACT TTCTAACTGG GATGTGGTAG AGGGACTGAA GGTACCTTTG
2251 GGGGCAACAG CACCTTAGTT TCATTCTCAA CTCTAGCCCT GCACACTCAC
2301 CTGTGGCAGC GAATGAAAAC AGAGCTTCCC GTGCAAAAAG GGTACAGCCT
2351 CCCACCCCCG CCCCCTCCCT GCACCTCCTG TCCTCTCCCA GTTCATTCTC
2401 GGAACCAGCC AGGCCAGGCA ACCAGTGGCC CCCAAAGGCA GGCAGGATCC
2451 TCAGGCCCCA GCCGCGGGAG GCTGGAAGGG CTGGCAGATC GCTTCCCTCA
2501 TCCACCTCCA CCGGTCCAGG TCTTTGCTGC TGTCCCCAGA CCTCCTGTGA
2551 CACCACGCCA GATCACAGGG CACCAGGCCA GAGATAGTCT TCTTTTTGTC
2601 CTTTCTGGCC TCTGGCTAGT CAGTTTTTCA TAGCCTTACA GTATCTGGCT
2651 TTGTACTGAG AAATAAAACA CATTTTCATA AAAAAAAAAA AAAAAAAAAA
2701 AAAA

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FEATURES:

5' UTR: 1-93
 Start: 94-1506
 Stop: 1509
 3' UTR: 1510-2704

FIGURE 1, page 1 of 5

SPLICE FORM 2:

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1  TGGTTGAGGG AAGGGGCCGT GCCCGGTGCC AGCCCAGGTG CTCGCGGCCCT
51  GGCTCCATGG CCCTGGTCAC AGTGAGCCGT TCGCCCCCGG GCAGCGGCGC
101 CTCCACGCCC GTGGGGCCCT GGGACCAGGC GGTCCAGCGA AGGAGTCGAC
151 TCCAGCGAAG GCAGAGCTTT GCGGTGCTCC GTGGGGCTGT CCTGGGACTG
201 CAGGATGGAG GGGACAATGA TGATGCAGCA GAGGCCAGTT CTGAGCCAAC
251 AGAGAAGGCC CCGAGTGAGG AGGAGCTCCA CGGGGACCAG ACAGACTTCG
301 GGCAAGGATC CCAGAGTCCC CAGAAGCAGG AGGAGCAGAG GCAGCACCTG
351 CACCTCATGG TACAGCTGCT GAGGCCGAG GATGACATCC GCCTGGCAGC
401 CCAGCTGGAG GCACCCCGGC CTCCCCGGCT CCGCTACCTG CTGGTAGTTT
451 CTACACGAGA AGGAGAAGGT CTGAGCCAGG ATGAGACGGT CCTCCTGGGC
501 GTGGATTTC CTGACAGCAG CTCCCCAGC TGCACCCTGG GCCTGGTCTT
551 GCCCCTCTGG AGTGACACCC AGGTGTACTT AGATGGAGAC GGGGGCTTCA
601 GCGTGACGTC TGGTGGGCAA AGCCGGATCT TCAAGCCCAT CTCCATCCAG
651 ACCATGTGGG CCACACTCCA GGTATTGCAC CAAGCATGTG AGGCAGCTCT
701 AGGCAGCGGC CTTGTACCGG GTGGCAGTGC CCTCACCTGG GCCAGCCACT
751 ACCAGGAGAG ACTGAACTCC GAACAGAGCT GCCTCAATGA GTGGACGGCT
801 ATGGCCGACC TGGAGTCTCT GCGGCCTCCC AGCGCCGAGC CTGGCGGGTC
851 CTCAGAACAG GAGCAGATGG AGCAGGCGAT CCGTGCTGAG CTGTGGAAG
901 TGTTGGATGT CAGTGACCTG GAGAGTGTCA CTTCCAAAGA GATCCGCCAG
951 GCTCTGGAGC TGCGCCTGGG GCTCCCOCTC CAGCAGTACC GTGACTTCAT
1001 CGACAACCAG ATGCTGCTGC TGGTGGCACA GCGGGACCGA GCCTCCCGCA
1051 TCTTCCCCCA CCTCTACCTG GGCTCAGAGT GGAACGCAGC AAACCTGGAG
1101 GAGCTGCAGA GGAACAGGGT CACCCACATC TTGAACATGG CCCGGGAGAT
1151 TGACAAC TTCCTGAGC GCTTACCTA CCACAATGTG CGCCTCTGGG
1201 ATGAGGAGTC GGCCCAGCTG CTGCCGCACT GGAAGGAGAC GCACCGCTTC
1251 ATTGAGGCTG CAAGAGCACA GGGCACCCAC GTGCTGGTCC ACTGCAAGAT
1301 GGGCGTCAGC CGCTCAGCGG CCACAGTGCT GGCCTATGCC ATGAAGCAGT
1351 ACGAATGCAG CCTGGAGCAG GCCCTGCGCC ACGTGCAGGA GCTCCGGCCC
1401 ATCGCCCCGC CCAACCCTGG CTTCTGCGC CAGCTGCAGA TCTACCAGGG
1451 CATCCTGACG GCCAGCCGCC AGAGCCATGT CTGGGAGCAG AAAGTGGGTG
1501 GGGTCTCCCC AGAGGAGCAC CCAGCCCTG AAGTCTCTAC ACCATTCCCA
1551 CTTCTTCCGC CAGAACCTGA GGGTGGTGGG GAGGAGAAGG TTGTAGGCAT
1601 GGAAGAGAGC CAGGCAGCCC CGAAAGAAGA GCCTGGGCCA CGGCCACGTA
1651 TAAACCTCCG AGGGGT CATG AGGTCCATCA GTCTTCTGGA GCCCTCCTTG
1701 GAGCTGGAGA GCACCTCAGA GACCAGTGAC ATGCCAGAGG TCTTCTCTTC
1751 CCACGAGTCT TCACATGAAG AGCCTCTGCA GCCCTTCCCA CAGCTTGCAA
1801 GGACCAAGGG AGGCCAGCAG GTGGACAGGG GGCCTCAGCC TGCCCTGAAG
1851 TCCCGCCAGT CAGTGGTTC CCTCCAGGGC AGTGCCGTGG TGGCCAACCG
1901 GACCCAGGCC TTCCAGGAGC AGGAGCAGGG GCAGGGGCAG GGGCAGGGAG
1951 AGCCCTGCAT TTCTCTACG CCCAGGTTCC GGAAGGTGGT GAGACAGGCC
2001 AGCGTG CATG ACAGTGGAGA GGAGGGCGAG GCCTGAGCCC TCACACATGC
2051 CCACGCTCCC CTGACACTGA AGAGGATCCA CAACTCCTTG GAGAAACACC
2101 CTCACGTCTG TTGCCGCACA CATTCTCTC AGCTCCGCC CATAACCGTC
2151 ACTACAGCCT CACCTCCAC CCCTGTCACT ACGGCCTCAC CTCCCACCCC
2201 TGTCACTACA GCCTCACCTC CTACAGCCTT AAGTCCCAGG CCCATGTCTG
2251 CCTGTCCAAG GGCTCAAGAC TTTCTAACTG GGATGTGGTA GAGGGACTGA
2301 AGGTACCTTT GGGGGCAACA GCACCCTAGT TTCATTCTCA ACTCTAGCCC
2351 TGCACACTCA CCTGTGGCAC GGAATGAAAA CAGAGCTTCC CGTGCAAAAA
2401 GGGTCACGCC TCCCACCCC GCCCCTCCC TGCACCTCCT GTCCTCTCCC
2451 AGTTCATTCC TGGAAACCAGC CAGGCCAGGC AACCAGTGGC CCCCAAAGGC
2501 AGGCAGGATC CTCAGGCCCC AGCCGCGGGA GGCTGGAAGG GCTGGCAGAT
2551 CGCTTCCCTC ATCCACCTCC ACCGCTCCAG GTCTTTGCTG CTGTCCCAG
2601 ACCTCCTGTG ACACCAGGCC AGATCACAGG GCACCAGGCC AGAGATAGTC
2651 TTCTTTTGT CTTTCTGGC CTCTGGCTAG TCAGTTTTTC ATAGCCTTAC
2701 AGTATCTGGC TTTGTACTGA GAAATAAAAC ACATTTTCAT AAAAAAAAAA
2751 AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA
2801 AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA
2851 AA

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FIGURE 1, page 2 of 5

FEATURES:

5' UTR: 1-56
 Start: 57
 Stop: 2034
 3' UTR: 2037-2852

SPLICE FORM 3:

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1  CCTGGTCCTG CCGGTCCAGG ACTGTCCCGC GGGGTTGAGG GAAGGGGCCG
51  TGCCCCGTGC CAGCCCAGGT GCTCGCGGCC TGGCTCCATG GCCCTGGTCA
101 CAGTGAGCCG TTCGCCCCCG GGCAGCGGCG CCTCCACGCC CGTGGGGCCC
151 TGGGACCAGG CCGTCCAGCG AAGGAGTCGA CTCCAGCGAA GGCAGAGCTT
201 TGCGGTGCTC CGTGGGGCTG TCCTGGGACT GCAGGATGGA GGGGACAATG
251 ATGATGCAGC AGAGGCCAGT TCTGAGCCAA CAGAGAAGGC CCCGAGTGAG
301 GAGGAGCTCC ACGGGGACCA GACAGACTTC GGGCAAGGAT CCCAGAGTCC
351 CCAGAAGCAG GAGGAGCAGA GGCAGCACCT GCACCTCATG GTACAGCTGC
401 TGAGGCCGCA GGATGACATC CGCCTGGCAG CCCAGCTGGA GGCACCCCGG
451 CCTCCCCGGC TCCGCTACCT GCTGGTAGTT TCTACACGAG AAGGAGAAGG
501 TCTGAGCCAG GATGAGACGG TCCTCCTGGG CGTGGATTTC CCTGACAGCA
551 GCTCCCCCAG CTGCACCCTG GGCCTGGTCT TGCCCCCTCT GAGTGACACC
601 CAGGTGTACT TAGATGGAGA CGGGGGCTTC AGCGTGACGT CTGGTGGGCA
651 AAGCCGGATC TTCAAGCCCA TCTCCATCCA GACCATGTGG TCCTCAGAAC
701 AGGAGCAGAT GGAGCAGCGG ATCCGTGCTG AGCTGTGGAA AGTGTGGGAT
751 GTCAGTGACC TGGAGAGTGT CACTTCCAAA GAGATCCGCC AGGCTCTGGA
801 GCTGCGCCTG GGGCTCCCCC TCCAGCAGTA CCGTGACTTC ATCGACAACC
851 AGATGCTGCT GCTGGTGGCA CAGCGGGACC GAGCCTCCCG CATCTTCCCC
901 CACCTCTACC TGGGCTCAGA GTGGAACGCA GCAAACCTGG AGGAGCTGCA
951 GAGGAACAGG GTCACCACA TCTTGAACAT GGCCCGGAG ATTGACAACT
1001 TCTACCCTGA GCGCTTCACC TACCACAATG TGCGCCTCTG GGATGAGGAG
1051 TCGGCCCAGC TGCTGCCGCA CTGGAAGGAG ACGCACCGCT TCATTGAGGC
1101 TGCAAGAGCA CAGGGCACCC ACGTGTGGT CCACTGCAAG ATGGGCGTCA
1151 GCGCTCAGC GGCCACAGTG CTGGCCTATG CCATGAAGCA GTACGAATGC
1201 AGCCTGGAGC AGGCCCTGCG CCACGTGCAG GAGTCCGGC CCATCGCCCG
1251 CCCCACCCTT GGCTTCCTGC GCCAGCTGCA GATCTACCAG GGCATCCTGA
1301 CGGCCAGAAC CTGAGGGTGG TGGGGAGGAG AAGSTTGTAG GCATGGAAGA
1351 GAGCCAGGCA GCGCTTCAAG AAGAGCCTGG GGCCACGGGG CACGTATAAA
1401 CCTCCGAGGG GTCATGAGGT CCATCAGTCT TCTGGAGCCC TCCTTGGGAG
1451 CTGGAGAGCA CCTCAGTAGA CCACTGACAT GCCAGAGGTC TTCTCTTCCC
1501 ACGAGTCTTC ACATGAAGAG CCTCTGCAGC CCTTCCACA GCTTGCAAGG
1551 ACCAAGGGAG GCCAGCAGGT GGACAGGGGG CCTCAGCCTG CCCTGAAGTC
1601 CCGCCAGTCA GTGGTTACCC TCCAGGGCAG TGCCGTGGTG GCCAACCGBA
1651 CCCAGGCCTT CCAGGAGCAG GAGCAGGGGC AGGGGCAGGG GCAGGGAGAG
1701 CCCTGCATTT CCTCTACGCC CAGGTTCCGG AAGGTGGTGA GACAGGCCAG
1751 CGTGCATGAC AGTGGAGAGG AGGGCGAGGC CTGAGCCCTC ACACATGCCC
1801 ACGTCCCCCT GACACTGAAG AGGATCCACA ACTCCTTGA GAAACACCCT
1851 CACGTCTGTT GCCGCACACA TTCCTCTCAG CTCCGCCCCA TACCCGTAC
1901 TACAGCCTCA CCTCCCACCC CTGTCACTAC GGCCTCACCT CCCACCCCTG
1951 TCACTACAGC CTCACCTCCT ACAGCCTTAA GTCCCAGGCC CATGTCTGCC
2001 TGTCCAAGGG CTCAAGACTT TCTAACTGGG ATGTGGTAGA GGGACTGAAG
2051 GTACCTTTGG GGGCAACAGC ACCCTAGTTT CATTCTCAAC TCTAGCCCTG
2101 CACACTCACC TGTGGCACGG AATGAAAACA GAGCTTCCCG TGCAAAAAGG
2151 GTCACGCCTC CCACCCCGC CCCCTCCCTG CACCTCCTGT CCTCTCCCAG
2201 TTCATTCCCTG GAACCAGCCA GGCCAGGCAA CCAGTGGCCC CCAAAGGCAG
2251 GCAGGATCCT CAGGCCCCAG CCGCGGGAGG CTGGAAGGGC TGGCAGATCG
2301 CTTCCCTCAT CCACCTCCAC CGGTCCAGGT CTTTGCTGCT GTCCCCAGAC
2351 CTCCTGTGAC ACCACGCCAG ATCACAGGGC ACCAGGCCAG AGATAGTCTT
2401 CTTTTTGTCC TTTCTGGCCT CTGGCTAGTC AGTTTTTCAT AGCCTTACAG
2451 TATCTGGCTT TGTACTGAGA AATAAAACAC ATTTTCATAT TTGGTTAAAA
2501 AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA
  
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FEATURES:
 5' UTR: 1-88
 Start: 88
 Stop: 1311
 3' UTR: 1315-2540

Homologous proteins:

Top 10 BLAST Hits

	Score	E
SPLICE FORM 1:		
gi 8923483 ref NP_060327.1 hypothetical protein FLJ20515 >gi 7...	576	e-163
gi 6714641 dbj BAA89534.1 (AB036834) MAP kinase phosphatase [D...	337	2e-91
gi 8922777 ref NP_060746.1 hypothetical protein FLJ10928 >gi 7...	233	3e-60
gi 7242951 dbj BAA92536.1 (AB037719) KIAA1298 protein [Homo sa...	143	4e-33
gi 7301242 gb AAF56372.1 (AE003750) CG6238 gene product [Droso...	124	2e-27
gi 4150963 emb CAA77232.1 (Y18620) DsPTP1 protein [Arabidopsis...	113	5e-24
gi 9294518 dbj BAB02780.1 (AB023036) dual-specificity protein ...	113	5e-24
gi 6862915 gb AAF30304.1 AC018907_4 (AC018907) putative dual-sp...	94	2e-18
gi 6015037 sp O54838 DUS5_RAT DUAL SPECIFICITY PROTEIN PHOSPHAT...	92	9e-18
gi 9910432 ref NP_064570.1 mitogen-activated protein kinase ph...	90	3e-17

SPLICE FORM 2:

gi 8923483 ref NP_060327.1 hypothetical protein FLJ20515 [Homo...	576	e-163
gi 6714641 dbj BAA89534.1 (AB036834) MAP kinase phosphatase [D...	340	6e-92
gi 8922777 ref NP_060746.1 hypothetical protein FLJ10928 [Homo...	229	1e-58
gi 7242951 dbj BAA92536.1 (AB037719) KIAA1298 protein [Homo sa...	162	1e-38
gi 9294518 dbj BAB02780.1 (AB023036) dual-specificity protein ...	113	8e-24
gi 4150963 emb CAA77232.1 (Y18620) DsPTP1 protein [Arabidopsis...	113	8e-24
gi 4758212 ref NP_004411.1 dual specificity phosphatase 8 [Hom...	99	3e-19
gi 6679156 ref NP_032774.1 neuronal tyrosine/threonine phosphat...	96	2e-18
gi 6862915 gb AAF30304.1 AC018907_4 (AC018907) putative dual-sp...	94	6e-18
gi 6015037 sp O54838 DUS5_RAT DUAL SPECIFICITY PROTEIN PHOSPHAT...	92	2e-17

SPLICE FORM 3:

gi 8923483 ref NP_060327.1 hypothetical protein FLJ20515 [Homo...	410	e-113
gi 8922777 ref NP_060746.1 hypothetical protein FLJ10928 [Homo...	233	7e-60
gi 6714641 dbj BAA89534.1 (AB036834) MAP kinase phosphatase [D...	224	5e-57
gi 7242951 dbj BAA92536.1 (AB037719) KIAA1298 protein [Homo sa...	143	5e-33
gi 9294518 dbj BAB02780.1 (AB023036) dual-specificity protein ...	113	1e-23
gi 4150963 emb CAA77232.1 (Y18620) DsPTP1 protein [Arabidopsis...	113	1e-23
gi 6862915 gb AAF30304.1 AC018907_4 (AC018907) putative dual-sp...	94	5e-18
gi 6015037 sp O54838 DUS5_RAT DUAL SPECIFICITY PROTEIN PHOSPHAT...	92	2e-17
gi 9910432 ref NP_064570.1 mitogen-activated protein kinase ph...	90	7e-17
gi 9911130 gb AAA64693.2 (U15932) protein phosphatase [Homo sa...	90	1e-16

BLAST to dbEST:

SPLICE FORM 1:

	Score	E
gi 9807071 /dataset=dbest /taxon=960...	1404	0.0
gi 10317998 /dataset=dbest /taxon=96...	1316	0.0
gi 10151079 /dataset=dbest /taxon=96...	1249	0.0
gi 10401153 /dataset=dbest /taxon=960...	1180	0.0
gi 10329921 /dataset=dbest /taxon=96...	1124	0.0
gi 7632969 /dataset=dbest /taxon=960...	791	0.0
gi 9155111 /dataset=dbest /taxon=9606...	779	0.0
gi 10994242 /dataset=dbest /taxon=96...	450	e-124

EXPRESSION INFORMATION FOR MODULATORY USE:

SPLICE FORM 1:

library source:

Expression information from BLAST dbEST hits:

gi 9807071	Human Pancreas
gi 10317998	Human colon adenocarcinoma
gi 10151079	Human Pancreas:adenocarcinoma
gi 10401153	Human Pancreas:epithelioid carcinoma
gi 10329921	Human lung: large cell carcinoma
gi 7632969	Human kidney: renal cell carcinoma
gi 9155111	Human Placenta choriocarcinoma
gi 10994242	Human ovary tumor tissue

Expression information from PCR-based tissue screening panels:

Human Brain
Human Fetal brain
Human fetal heart
Human fetal kidney
Human heart
Human kidney
Human uterus
Human thyroid

SPLICE FORM 1:

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1 MALVTVSRSP PGSGASTPVG PWDQAVQRRS RLQRRQSFAV LRGAVLGLQD
51 GGDNDAAEA SSEPTEKAPS EEELHGDQTD FGQGSQSPQK QEEQRQHLHL
101 MVQLLRPQDD IRLAAQLEAP RPPRLRYLLV VSTREGEGLS QDET VLLGVD
151 FPDSSSPSCT LGLVLPLWSD TQVYLDGDGG FSVTSGGQSR IFKPISIQTM
201 WATLQVLHQA CEALGSGLV PGGSALTWAS HYQERLNSEQ SCLNEWTAMA
251 DLESLRPPSA EPGGSSESEQ MEQAIRAELW KVLVDSDLES VTSKEIRQAL
301 ELRLGLPLQQ YRDFIDNQML LLVAQRDRAS RIFPHLYLGS EWNAANLEEL
351 QRNRVTHILN MAREIDNFYP ERFTYHNVRL WDEESAQLLP HWKETHRFIE
401 AARAQGTHVL VHCKMGVSRs AATVLAYAMK QYECsLEQAL RHVQELRPIA
451 RPNPGFLRQL QIYQGILTAR T
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SPLICE FORM 2:

```
1 MALVTVSRSP PGSGASTPVG PWDQAVQRRS RLQRRQSFAV LRGAVLGLQD
51 GGDNDAAEA SSEPTEKAPS EEELHGDQTD FGQGSQSPQK QEEQRQHLHL
101 MVQLLRPQDD IRLAAQLEAP RPPRLRYLLV VSTREGEGLS QDET VLLGVD
151 FPDSSSPSCT LGLVLPLWSD TQVYLDGDGG FSVTSGGQSR IFKPISIQTM
201 WATLQVLHQA CEALGSGLV PGGSALTWAS HYQERLNSEQ SCLNEWTAMA
251 DLESLRPPSA EPGGSSESEQ MEQAIRAELW KVLVDSDLES VTSKEIRQAL
301 ELRLGLPLQQ YRDFIDNQML LLVAQRDRAS RIFPHLYLGS EWNAANLEEL
351 QRNRVTHILN MAREIDNFYP ERFTYHNVRL WDEESAQLLP HWKETHRFIE
401 AARAQGTHVL VHCKMGVSRs AATVLAYAMK QYECsLEQAL RHVQELRPIA
451 RPNPGFLRQL QIYQGILTAS RQSHVWEQKV GGVsPEEHPA PEVSTPFPLL
501 PPEPEGGEGE KVVGMESQA APKEEPGPRP RINLRGVMRS ISLLEPSLEL
551 ESTSETSDMP EVFSSHESH EEPLQPPFQL ARTKGGQQVD RGPQPALKSR
601 QSVVTLQGSA VVANRTQAFQ EQEQGQGQGQ GEPCISSTPR FRKVVRQASV
651 HDSGEEGEA
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SPLICE FORM 3:

```
1 MALVTVSRSP PGSGASTPVG PWDQAVQRRS RLQRRQSFAV LRGAVLGLQD
51 GGDNDAAEA SSEPTEKAPS EEELHGDQTD FGQGSQSPQK QEEQRQHLHL
101 MVQLLRPQDD IRLAAQLEAP RPPRLRYLLV VSTREGEGLS QDET VLLGVD
151 FPDSSSPSCT LGLVLPLWSD TQVYLDGDGG FSVTSGGQSR IFKPISIQTM
201 WSSEQEQMEQ AIRAELWKVL DVSDLESVTS KEIRQALELR LGLPLQQYRD
251 FIDNQMLLLV AQDRASRIF PHLYLGSEWN AANLEELQRN RVTHILNMAR
301 EIDNFYPERF TYHNVRLWDE ESAQLLPHWK ETHRFIEAAR AQGTHVLVHC
351 KMGVSRSAAT VLAYAMKQYE CSLEQALRHV QELRPIARPN PGFLRQLQIY
401 QGILTART
```

FEATURES:**Functional domains and key regions:****SPLICE FORM 1:**

[1] PDOC00004 PS00004 CAMP_PHOSPHO_SITE

cAMP- and cGMP-dependent protein kinase phosphorylation site

34-37 RRQS

[2] PDOC00005 PS00005 PKC_PHOSPHO_SITE

Protein kinase C phosphorylation site

Number of matches: 6

1	65-67	TEK
2	132-134	STR
3	254-256	SLR
4	292-294	TSK
5	395-397	THR
6	468-470	TAR

[3] PDOC00006 PS00006 CK2_PHOSPHO_SITE
Casein kinase II phosphorylation site

Number of matches: 6

1	70-73	SEEE
2	132-135	STRE
3	140-143	SQDE
4	266-269	SEQE
5	286-289	SDLE
6	292-295	TSKE

[4] PDOC00007 PS00007 TYR_PHOSPHO_SITE
Tyrosine kinase phosphorylation site

363-369 REIDNFY

[5] PDOC00008 PS00008 MYRISTYL
N-myristoylation site

Number of matches: 8

1	12-17	GSGAST
2	43-48	GAVLGL
3	47-52	GLQDGG
4	218-223	GLVPGG
5	223-228	GSALTW
6	339-344	GSEWNA
7	416-421	GVSRSA
8	465-470	GILTAR

BLAST Alignment to Top Hit:

SPLICE FORM 1:

>gi|8923483|ref|NP_060327.1| hypothetical protein FLJ20515
 >gi|7020674|dbj|BAA91228.1| (AK000522) unnamed protein
 product [Homo sapiens]
 Length = 394

Score = 576 bits (1469), Expect = e-163
 Identities = 290/312 (92%), Positives = 296/312 (93%), Gaps = 1/312 (0%)

Query: 1 MALVTVSRSPPGSGASTPVGPWDQAVQRRSRLQRRQSFAVLRGAVLGLQDGGDNDDAAEA 60
 MALVTVSRSPPGSGASTPVGPWDQAVQRRSRLQRRQSFAVLRGAVLGLQDGGDNDDAAEA
 Sbjct: 1 MALVTVSRSPPGSGASTPVGPWDQAVQRRSRLQRRQSFAVLRGAVLGLQDGGDNDDAAEA 60

Query: 61 SSEPTEKAPSEELHGDQTDGFGGSQSPQKQEEQRQHLHLMVQLLRPQDDIRLAAQLEAP 120
 SSEPTEKAPSEELHGDQTDGFGGSQSPQKQEEQRQHLHLMVQLLRPQDDIRLAAQLEAP
 Sbjct: 61 SSEPTEKAPSEELHGDQTDGFGGSQSPQKQEEQRQHLHLMVQLLRPQDDIRLAAQLEAP 120

Query: 121 RPPRLRYLLVVSTREGEGLSQDETIVLLGVDFPDSSSPSCTLGLVPLWSDTQVYLDGDGG 180
 RPPRLRYLLVVSTREGEGLSQDETIVLLGVDFPDSSSPSCTLGLVPLWSDTQVYLDGDGG
 Sbjct: 121 RPPRLRYLLVVSTREGEGLSQDETIVLLGVDFPDSSSPSCTLGLVPLWSDTQVYLDGDGG 180

Query: 181 FSVTSGGQSRIFKPISIQTMWATLQVLHQACEAALGSLVPGGSALTWASHYQERLNSEQ 240
 FSVTSGGQSRIFKPISIQTMWATLQVLHQACEAALGSLVPGGSALTWASHYQERLNSEQ
 Sbjct: 181 FSVTSGGQSRIFKPISIQTMWATLQVLHQACEAALGSLVPGGSALTWASHYQERLNSEQ 240

Query: 241 SCLNEWTAMADLES LRPPSAEPGGSSEQE QMEQAIRAELWKVLDV-SDLESVTSKEIRQA 299
 SCLNEWTAMADLES LRPPSAEPGGSSEQE QMEQAIRAELWKVL++ S E+ E+ +
 Sbjct: 241 SCLNEWTAMADLES LRPPSAEPGGSSEQE QMEQAIRAELWKVLELESTSETSDMPEVFSS 300

Query: 300 LELRLGLPLQOY 311
 E PLQ +
 Sbjct: 301 HESSHEEPLQPF 312

>gi|6714641|dbj|BAA89534.1| (AB036834) MAP kinase phosphatase
 [Drosophila melanogaster]
 Length = 1045

Score = 337 bits (854), Expect = 2e-91
 Identities = 204/537 (37%), Positives = 284/537 (51%), Gaps = 81/537 (15%)

Query: 1 MALVTVSRSPPGSGA-STPVGPWDQAVQRRSRLQRRQSFAVLRGAVLGLQDGGDNDDAAE 59
 MALVTV RSP +G+ S G + R + F +G L L
 Sbjct: 1 MALVTVQRSPSVAGSCSNDSGESEDDGNSKGNDRSECFAGKGTALVL----- 49

Query: 60 ASSEPTEKAPSEELHGDQTDGFGGSQSPQKQEEQRQHLHLMVQLLRPQDDIRLAAQLEA 119
 A + SE L D T +QS + + HL M LL+ +D +++A +LE+
 Sbjct: 50 ALKDIPPLTQSERRLSTDSTRSSNSTQS--NNSDIQLHLQSMFYLLQREDTLKMAVKLES 107

Query: 120 PRPPRLRYLLV-----VSTREGEGLSQDETIVLLGVDFPDSSSPS----- 158
 R R RYL++ S R + + +V +G SS S
 Sbjct: 108 QRSNRTRYLVIA SRCCRS GTS DRRRHRIMRHHSVKVGG SAGTKSSTSPAVPTQRQLSVE 167

Query: 159 -----CTLGL-----VLPLWSDTQVY 174
 C LG+ V+P+ +DT ++
 Sbjct: 168 QTATEASSKCDKTADKENATAAGDNKNTSGMEESCLLGIDCNERTTIGLVVPILADTTIH 227

Query: 175 LDGDGGFSVTSGGQSRIFKPISIQTMWATLQVLHQACEAALGSLVPGGSALTWASHYQE 234
 LDGDGGFSV ++ IFKP+S+Q MW+ LQ LH+ + A + G + W S Y+
 Sbjct: 228 LDGDGGFSVKVYEKTHIFKPVSVQAMWSALQTLHKVSKKAREN NFYASGPSHDWLSSYER 287

Query: 235 RLNSEQSCLNEW TAMADLES LRPPSAEP--GGSSSEQEQMEQAIRAELWKVLDVSDLESVT 292
R+ S+QSCLNEW AM LES RPPS + E+E+ E I+ +L ++ DL+ VT
Sbjct: 288 RIESDQSCLNEW NAMDALESRRPPSPDAIRNKPPEKEETESVIKMKLKAIMMSVDLDEVT 347

Query: 293 SKEIRQALELRLGLPLQYRDFIDNQMLLLVAQRDRASRIFPHLYLGSEWNAANLEELQR 352
SK IR LE L + L +Y+ FID +ML+++ Q D ++IF H+YLGSEWNA+NLEELQ+
Sbjct: 348 SKYIRGRLEEILDMDLGEYKSFIDAEMLVILGQMDAPTKIFEHVYLGSEWNASNLEELQK 407

Query: 353 NRVTHILNMAREIDNFYPERFTYHNVRWLWDEESAQLLPHWKETHRFIEAARAQGTHVLVH 412
N V HILN+ REIDNF+P F Y NVR++D+E LL +W +T R+I A+A+G+ VLVH
Sbjct: 408 NGVRHILNVTREIDNFFPGTFEYFNVRVYDDEKTNLLKYWDDTFRYITRAKAEGSKVLVH 467

Query: 413 CKMGVSRSAATVLAYAMKQYEC SLEQALRHVQELRPIARP NPGFLRQLQIYQGILTA 469
CKMGVSRSA+ V+AYAMK Y+ +QAL HV++ R +PN FL QL+ Y G+L A
Sbjct: 468 CKMGVSRASVVIAYAMKAYQWEFQQALEHVKKRRSCIKPNKNFLNQLETYSGLMDA 524

>gi|8922777|ref|NP_060746.1| hypothetical protein FLJ10928
>gi|7023283|dbj|BAA91913.1| (AK001790) unnamed protein
product [Homo sapiens]
Length = 141

Score = 233 bits (588), Expect = 3e-60
Identities = 111/111 (100%), Positives = 111/111 (100%)

Query: 361 MAREIDNFYPERFTYHNVRWLWDEESAQLLPHWKETHRFIEAARAQGTHVLVHCKMGVSRS 420
MAREIDNFYPERFTYHNVRWLWDEESAQLLPHWKETHRFIEAARAQGTHVLVHCKMGVSRS
Sbjct: 31 MAREIDNFYPERFTYHNVRWLWDEESAQLLPHWKETHRFIEAARAQGTHVLVHCKMGVSRS 90

Query: 421 AATVLAYAMKQYEC SLEQALRHVQELRPIARP NPGFLRQLQIYQGILTART 471
AATVLAYAMKQYEC SLEQALRHVQELRPIARP NPGFLRQLQIYQGILTART
Sbjct: 91 AATVLAYAMKQYEC SLEQALRHVQELRPIARP NPGFLRQLQIYQGILTART 141

1 CGTCCTTCCT GGTCTGCGG GTCCAGGACT GTCCGCGGG TTGAGGGAAG
 51 GGGCCGTGCC CGGTGCCAGC CCAGGTGCTC GCGGCTGGC TCCATGGCCC
 101 TGGTCACAGT GAGCCGTTCG CCCCCGGGCA GCGGCGCCTC CACGCCCGTG
 151 GGGCCCTGGG ACCAGGCGGT CCAGCGAAGG AGTCGACTCC AGCGAAGGCA
 201 GAGCTTTGCG GTGCTCCGTG GGGCTGTCTT GGGACTGCAG GATGGAGGGG
 251 ACAATGATGA TGCAGCAGAG GCCAGTTCTG AGCCAACAGA GAAGGCCCCG
 301 AGTGAGGAGG AGCTCCACGG GGACCAGACA GACTTCGGGC AAGGATCCCA
 351 GAGTCCCCAG AAGCAGGAGG AGCAGAGGCA GCACCTGCAC CTCATGGTAC
 401 AGCTGCTGAG GCCGCAGGAT GACATCCGCC TGGCAGCCCA GCTGGAGGCA
 451 CCCCggcctc CCGGCTCCG CTACCTGCTG GTAGTTTCTA CACGAGAAGG
 501 AGAAGGTCTG AGCCAGGATG AGACGGTCCT CCTGGGCGTG GATTTCCCTG
 551 ACAGCAGCTC CCCCAGCTGC ACCCTGGGCC TGGTCTTGCC CCTCTGGAGT
 601 GACACCCAGG TGTACTTAGA TGGAGACGGG GGCTTCAGCG TGACGTCTGG
 651 TGGGCAAAGC CGGATCTTCA AGCCCATCTC CATCCAGACC ATGTGGGCCA
 701 CACTCCAGGT ATTGCACCAA GCATGTGAGG CAGCTCTAGG CAGCGGCCTT
 751 GTACCGGGTG GCAGTGCCCT CACCTGGGCC AGCCACTACC AGGAGAGACT
 801 GAACCTCCGA CAGAGCTGCC TCAATGAGTG GACGGCTATG GCCGACCTGG
 851 AGTCTCTGCG GCCTCCCAGC GCCGAGCCTG GCGGGTCCTC AGAACAGGAG
 901 CAGATGGAGC AGGCGATCCG TGCTGAGCTG TGGAAAGTGT TGGATGTCAG
 951 TGACCTGGAG AGTGTCACTT CCAAAGAGAT CCGCCAGGCT CTGGAGCTGC
 1001 GCCTGGGGCT CCCCCTCCAG CAGTACCGTG ACTTCATCGA CAACCAGATG
 1051 CTGCTGCTGG TGGCACAGCG GGACCGAGCC TCCCGCATCT TCCCCACCT
 1101 CTACCTGGGC TCAGAGTGGA ACGCAGCAAA CCTGGAGGAG CTGCAGAGGA
 1151 ACAGGGTCAC CCACATCTTG AACATGGCCC GGGAGATTGA CAACTTCTAC
 1201 CCTGAGCGCT TCACCTACCA CAATGTGCGC CTCTGGGATG AGGAGTCGGC
 1251 CCAGTGCTG CCGCACTGGA AGGAGACGCA CCGCTTCATT GAGGCTGCAA
 1301 GAGCACAGGG CACCACAGTG CTGGTCCACT GCAAGATGGG CGTCAGCCGC
 1351 TCAGCGGCCA CAGTGCTGGC CTATGCCATG AAGCAGTACG AATGCAGCCT
 1401 GGAGCAGGCC CTGCGCCACG TGCAGGAGCT CCGGCCATC GCCCGCCCA
 1451 ACCCTGGCTT CCTGCGCCAG CTGCAGATCT ACCAGGGCAT CCTGACGGCC
 1501 AGAACCTGAG GGTGGTGGGG AGGAGAAGGT TGTAGGCATG GAAGAGAGCC
 1551 AGGCAGCCCC GAAAGAAGAG CCTGGGCCAC GGCCACGTAT AAACCTCCGA
 1601 GGGGTTCATGA GGTCCATCAG TCTTCTGGAG CCTCCTTGG AGCTGGAGAG
 1651 CACCTCAGAG ACCAGTGACA TGCCAGAGGT CTTCTCTTCC CACGAGTCTT
 1701 CACATGAAGA GCCTCTGCAG CCCTTCCCAC AGCTTGCAAG GACCAAGGGA
 1751 GGCCAGCAGG TGGACAGGGG GCCTCAGCCT GCCCTGAAGT CCCGCCAGTC
 1801 AGTGGTTACC CTCCAGGGCA GTGCCGTGGT GGCCAACCGG ACCCAGGCCT
 1851 TCCAGGAGCA GGAGCAGGGG CAGGGGCAGG GGCAGGGAGA GCCCTGCATT
 1901 TCCTCTACGC CCAGGTTCGG GAAGGTGGTG AGACAGGCCA GCGTGCATGA
 1951 CAGTGGAGAG GAGGGCAGAG CCTGAGCCCT CACACATGCC CACGCTCCCC
 2001 TGACACTGAA GAGGATCCAC AACTCCTTGG AGAAACACCC TCACGTCTGT
 2051 TGCCGCACAC ATTCTCTCA GCTCCGCCCC ATACCCGTCA CTACAGCCTC
 2101 ACCTCCCACC CTTGTCACTA CGGCCTCACC TCCCACCCCT GTCACACAG
 2151 CCTCACCTCC TACAGCCTTA AGTCCCAGGC CCATGTCTGC CTGTCCAAGG
 2201 GCTCAAGACT TTCTAACTGG GATGTGGTAG AGGGACTGAA GGTACCTTTG
 2251 GGGGCAACAG CACCCTAGTT TCATTCTCAA CTCTAGCCCT GCACACTCAC
 2301 CTGTGGCAGC GAATGAAAAC AGAGCTTCCC GTGCAAAAAG GGTACAGCCT
 2351 CCCACCCCCG CCCCCTCCCT GCACCTCCTG TCCTCTCCCA GTTCATTCTT
 2401 GGAACCAGCC AGGCCAGGCA ACCAGTGGCC CCCAAAGGCA GGCAGGATCC
 2451 TCAGGCCCCA GCCGCGGGAG GCTGGAAGGG CTGGCAGATC GCTTCCCTCA
 2501 TCCACCTCCA CCGGTCCAGG TCTTTGCTGC TGTCCCAGA CCTCCTGTGA
 2551 CACCACGCCA GATCACAGGG CACCAGGCCA GAGATAGTCT TCTTTTGTGTC
 2601 CTTTCTGGCC TCTGGCTAGT CAGTTTTCATA TAGCCTTACA GTATCTGGCT
 2651 TTGTACTGAG AAATAAAACA CATTTTCATA AAAAAAAAAA AAAAAAAAAA
 2701 AAAA

FEATURES:

Start: 94
 Exon: 94-1506
 Stop: 1507

FIGURE 3, page 1 of 8

CHROMOSOME MAP POSITION:
 Bac accession number: AP001885
 Chromosome #: 11

ALLELIC VARIANTS (SNPs):

DNA				Protein		
Position	Major	Minor	Domain	Position	Major	Minor
577	G	A	Exon	162	G	S
1451	G	A	Exon	453	S	N
2641	G	A	Beyond ORF(3')			

Context:

DNA

Position

577 TCTGAGCCAACAGAGAAGGCCCGAGTGAGGAGGAGCTCCACGGGGACCAGACAGACTTC
 GGGCAAGGATCCCAGAGTCCCCAGAAGCAGGAGGAGCAGAGGCAGCACCTGCACCTCATG
 GTACAGCTGCTGAGGCCGAGGATGACATCCGCCTGGCAGCCCAGCTGGAGGCACCCCGG
 CCTCCCCGGCTCCGCTACCTGCTGGTAGTTTCTACACGAGAAGGAGAAGGTCTGAGCCAG
 GATGAGACGGTCTCTGGGCGTGGATTTCCCTGACAGCAGCTCCCCCAGCTGCACCCCTG
 [G,A]
 GCCTGGTCTTGCCCCCTCTGGAGTGACACCCAGGTGTACTTAGATGGAGACGGGGGCTTCA
 GCGTGACGTCTGGTGGGCAAAGCCGGATCTTCAAGCCCATCTCCATCCAGACCATGTGGG
 CCACACTCCAGGTATTGCACCAAGCATGTGAGGCAGCTCTAGGCAGCGGCCTTGTACCGG
 GTGGCAGTGCCCTCACCTGGGCCAGCCACTACCAGGAGAGACTGAACTCCGAACAGAGCT
 GCCTCAATGAGTGGACGGCTATGGCCGACCTGGAGTCTCTGCGGCCTCCCAGCGCCGAGC

1451 ACAGGGTCACCCACATCTTGAACATGGCCCGGAGATTGACAACCTTCTACCCTGAGCGCT
 TCACCTACCACAATGTGCGCCTCTGGGATGAGGAGTCGGCCCAGCTGCTGCCGCACTGGA
 AGGAGACGCACCGCTTCATTGAGGCTGCAAGAGCACAGGGCACCACGTGCTGGTCCACT
 GCAAGATGGGCGTCAGCCGCTCAGCGGCCACAGTGCTGGCCTATGCCATGAAGCAGTACG
 AATGCAGCCTGGAGCAGGCCCTGCGCCACGTGCAGGAGCTCCGGCCCATCGCCCGCCCCA
 [G,A]
 CCCTGGCTTCTGCGCCAGCTGCAGATCTACCAGGGCATCCTGACGGCCAGAACCTGAGG
 GTGGTGGGGAGGAGAAGGTTGTAGGCATGGAAGAGAGCCAGGCAGCCCCGAAAGAAGAGC
 CTGGGCCACGGCCACGTATAAACCTCCGAGGGGTCTGAGGTCCATCAGTCTTCTGGAGC
 CCTCCTTGAGCTGGAGAGCACCTCAGAGACCAGTGACATGCCAGAGGTCTTCTCTTCCC
 ACGAGTCTTCACATGAAGAGCCTCTGCAGCCCTTCCACAGCTTGCAAGGACCAAGGGAG

2641 GGTACAGCCTCCCACCCCCGCCCCCTCCCTGCACCTCCTGTCTCTCCAGTTTCATTCCT
 GGAACCCAGCCAGGCCAGGCAACAGTGGCCCCCAAAGGCAGGCAGGATCCTCAGGCCCA
 GCCGCGGGAGGCTGGAAGGGCTGGCAGATCGCTTCCCTCATCCACCTCCACCGGTCCAGG
 TCTTTGCTGTGTCCCCAGACCTCCTGTGACACCAGCCAGATCACAGGGCACCAGGCCA
 GAGATAGTCTTCTTTTGTCTTTCTGGCCTCTGGCTAGTCAGTTTTTCATAGCCTTACA
 [G,A]
 TATCTGGCTTTGTACTGAGAAATAAAACACATTTTCATAAAAAAAAAAAAAAAAAAAAAA
 AAA

GENE STRUCTURE MODEL:

SPLICE FORM 2 5'-e1-e2-e3-e4-e5-e6-e7-e8-e9-e10-e11-e12-e13-e14-3'
 SPLICE FORM 1 5'-e1-e2-e3-e4-e5-e6-e7-e8-e9-e10-e11-e12-----3'
 SPLICE FORM 3 5'-e1-e2-e3-e4-e5-e6-----e8-e9-e10-e11-e12-----3'

MULTIPLE ALIGNMENT OF CDNA SEQUENCES:

SPLICE FORM 2 ~~~~~~TG GTTGAAGGAA
 SPLICE FORM 1 CGTCCTTCCT GGTCTGCGG GTCCAGGACT GT.CCGCGGG GTTGAAGGAA
 SPLICE FORM 3 ~~~~~~CCT GGTCTGCGG GTCCAGGACT GTCCCGCGG GTTGAAGGAA

51 100
 SPLICE FORM 2 GGGGCCGTGC CCGGTGCCAG CCCAGGTGCT CGCGGCCTGG CTCCATGGCC

FIGURE 3, page 2 of 8

SPLICE FORM 1 GGGGCCGTGC CCGGTGCCAG CCCAGGTGCT CGCGGCCTGG CTCCATGGCC
 SPLICE FORM 3 GGGGCCGTGC CCGGTGCCAG CCCAGGTGCT CGCGGCCTGG CTCCATGGCC

101 150

SPLICE FORM 2 CTGGTCACAG TGAGCCGTTT GGGCCCGGGC AGCGGCGCCT CCACGCCCCT
 SPLICE FORM 1 CTGGTCACAG TGAGCCGTTT GGGCCCGGGC AGCGGCGCCT CCACGCCCCT
 SPLICE FORM 3 CTGGTCACAG TGAGCCGTTT GGGCCCGGGC AGCGGCGCCT CCACGCCCCT

151 200

SPLICE FORM 2 GGGGCCCTGG GACCAGGCGG TCCAGCGAAG GAGTCGACTC CAGCGAAGGC
 SPLICE FORM 1 GGGGCCCTGG GACCAGGCGG TCCAGCGAAG GAGTCGACTC CAGCGAAGGC
 SPLICE FORM 3 GGGGCCCTGG GACCAGGCGG TCCAGCGAAG GAGTCGACTC CAGCGAAGGC

201 250

SPLICE FORM 2 AGAGCTTTGC GGTGCTCCGT GGGGCTGTCC TGGGACTGCA GGATGGAGGG
 SPLICE FORM 1 AGAGCTTTGC GGTGCTCCGT GGGGCTGTCC TGGGACTGCA GGATGGAGGG
 SPLICE FORM 3 AGAGCTTTGC GGTGCTCCGT GGGGCTGTCC TGGGACTGCA GGATGGAGGG

251 300

SPLICE FORM 2 GACAATGATG ATGCAGCAGA GGCCAGTTCT GAGCCAACAG AGAAGGCCCC
 SPLICE FORM 1 GACAATGATG ATGCAGCAGA GGCCAGTTCT GAGCCAACAG AGAAGGCCCC
 SPLICE FORM 3 GACAATGATG ATGCAGCAGA GGCCAGTTCT GAGCCAACAG AGAAGGCCCC

301 350

SPLICE FORM 2 GAGTGAGGAG GAGTCCACG GGGACCAGAC AGACTTCGGG CAAGGATCCC
 SPLICE FORM 1 GAGTGAGGAG GAGTCCACG GGGACCAGAC AGACTTCGGG CAAGGATCCC
 SPLICE FORM 3 GAGTGAGGAG GAGTCCACG GGGACCAGAC AGACTTCGGG CAAGGATCCC

351 400

SPLICE FORM 2 AGAGTCCCCA GAAGCAGGAG GAGCAGAGGC AGCACCTGCA CCTCATGGTA
 SPLICE FORM 1 AGAGTCCCCA GAAGCAGGAG GAGCAGAGGC AGCACCTGCA CCTCATGGTA
 SPLICE FORM 3 AGAGTCCCCA GAAGCAGGAG GAGCAGAGGC AGCACCTGCA CCTCATGGTA

401 450

SPLICE FORM 2 CAGCTGCTGA GGCCGCAGGA TGACATCCGC CTGGCAGCCC AGCTGGAGGC
 SPLICE FORM 1 CAGCTGCTGA GGCCGCAGGA TGACATCCGC CTGGCAGCCC AGCTGGAGGC
 SPLICE FORM 3 CAGCTGCTGA GGCCGCAGGA TGACATCCGC CTGGCAGCCC AGCTGGAGGC

451 500

SPLICE FORM 2 ACCCGGGCCT CCCCGGCTCC GCTACCTGCT GGTAGTTTCT ACACGAGAAG
 SPLICE FORM 1 ACCCGGGCCT CCCCGGCTCC GCTACCTGCT GGTAGTTTCT ACACGAGAAG
 SPLICE FORM 3 ACCCGGGCCT CCCCGGCTCC GCTACCTGCT GGTAGTTTCT ACACGAGAAG

501 550

SPLICE FORM 2 GAGAAGGTCT GAGCCAGGAT GAGACGGTCC TCCTGGGCGT GGATTTCCCT
 SPLICE FORM 1 GAGAAGGTCT GAGCCAGGAT GAGACGGTCC TCCTGGGCGT GGATTTCCCT
 SPLICE FORM 3 GAGAAGGTCT GAGCCAGGAT GAGACGGTCC TCCTGGGCGT GGATTTCCCT

551 600

SPLICE FORM 2 GACAGCAGCT CCCCCAGCTG CACCCTGGGC CTGGTCTTGC CCCTCTGGAG
 SPLICE FORM 1 GACAGCAGCT CCCCCAGCTG CACCCTGGGC CTGGTCTTGC CCCTCTGGAG
 SPLICE FORM 3 GACAGCAGCT CCCCCAGCTG CACCCTGGGC CTGGTCTTGC CCCTCTGGAG

601 650

SPLICE FORM 2 TGACACCCAG GTGTACTTAG ATGGAGACGG GGGCTTCAGC GTGACGTCTG
 SPLICE FORM 1 TGACACCCAG GTGTACTTAG ATGGAGACGG GGGCTTCAGC GTGACGTCTG
 SPLICE FORM 3 TGACACCCAG GTGTACTTAG ATGGAGACGG GGGCTTCAGC GTGACGTCTG

651 700

SPLICE FORM 2 GTGGGCAAAG CCGGATCTTC AAGCCCATCT CCATCCAGAC CATGTGGGCC
 SPLICE FORM 1 GTGGGCAAAG CCGGATCTTC AAGCCCATCT CCATCCAGAC CATGTGGGCC
 SPLICE FORM 3 GTGGGCAAAG CCGGATCTTC AAGCCCATCT CCATCCAGAC CATGT.....

FIGURE 3, page 3 of 8

701 750
SPLICE FORM 2 ACACTCCAGG TATTGCACCA AGCATGTGAG GCAGCTCTAG GCAGCGGCCT
SPLICE FORM 1 ACACTCCAGG TATTGCACCA AGCATGTGAG GCAGCTCTAG GCAGCGGCCT
SPLICE FORM 3
751 800
SPLICE FORM 2 TGTACCGGGT GGCAGTGCCC TCACCTGGGC CAGCCACTAC CAGGAGAGAC
SPLICE FORM 1 TGTACCGGGT GGCAGTGCCC TCACCTGGGC CAGCCACTAC CAGGAGAGAC
SPLICE FORM 3
801 850
SPLICE FORM 2 TGAACCTCGA ACAGAGCTGC CTCAATGAGT GGACGGCTAT GGCCGACCTG
SPLICE FORM 1 TGAACCTCGA ACAGAGCTGC CTCAATGAGT GGACGGCTAT GGCCGACCTG
SPLICE FORM 3
851 900
SPLICE FORM 2 GAGTCTCTGC GGCCTCCCAG CGCCGAGCCT GGCGGGTCCT CAGAACAGGA
SPLICE FORM 1 GAGTCTCTGC GGCCTCCCAG CGCCGAGCCT GGCGGGTCCT CAGAACAGGA
SPLICE FORM 3GGTCCT CAGAACAGGA
901 950
SPLICE FORM 2 GCAGATGGAG CAGGCGATCC GTGCTGAGCT GTGGAAAGTG TTGGATGTCA
SPLICE FORM 1 GCAGATGGAG CAGGCGATCC GTGCTGAGCT GTGGAAAGTG TTGGATGTCA
SPLICE FORM 3 GCAGATGGAG CAGGCGATCC GTGCTGAGCT GTGGAAAGTG TTGGATGTCA
951 1000
SPLICE FORM 2 GTGACCTGGA GAGTGTCCT TCCAAAGAGA TCCGCCAGGC TCTGGAGCTG
SPLICE FORM 1 GTGACCTGGA GAGTGTCCT TCCAAAGAGA TCCGCCAGGC TCTGGAGCTG
SPLICE FORM 3 GTGACCTGGA GAGTGTCCT TCCAAAGAGA TCCGCCAGGC TCTGGAGCTG
1001 1050
SPLICE FORM 2 CGCCTGGGGC TCCCCCTCCA GCAGTACCGT GACTTCATCG ACAACCAGAT
SPLICE FORM 1 CGCCTGGGGC TCCCCCTCCA GCAGTACCGT GACTTCATCG ACAACCAGAT
SPLICE FORM 3 CGCCTGGGGC TCCCCCTCCA GCAGTACCGT GACTTCATCG ACAACCAGAT
1051 1100
SPLICE FORM 2 GCTGCTGCTG GTGGCACAGC GGGACCGAGC CTCCCGCATC TTCCCCCACC
SPLICE FORM 1 GCTGCTGCTG GTGGCACAGC GGGACCGAGC CTCCCGCATC TTCCCCCACC
SPLICE FORM 3 GCTGCTGCTG GTGGCACAGC GGGACCGAGC CTCCCGCATC TTCCCCCACC
1101 1150
SPLICE FORM 2 TCTACCTGGG CTCAGAGTGG AACGCAGCAA ACCTGGAGGA GCTGCAGAGG
SPLICE FORM 1 TCTACCTGGG CTCAGAGTGG AACGCAGCAA ACCTGGAGGA GCTGCAGAGG
SPLICE FORM 3 TCTACCTGGG CTCAGAGTGG AACGCAGCAA ACCTGGAGGA GCTGCAGAGG
1151 1200
SPLICE FORM 2 AACAGGGTCA CCCACATCTT GAACATGGCC CGGGAGATTG ACAACTTCTA
SPLICE FORM 1 AACAGGGTCA CCCACATCTT GAACATGGCC CGGGAGATTG ACAACTTCTA
SPLICE FORM 3 AACAGGGTCA CCCACATCTT GAACATGGCC CGGGAGATTG ACAACTTCTA
1201 1250
SPLICE FORM 2 CCTGAGCGC TTCACCTACC ACAATGTGCG CCTCTGGGAT GAGGAGTCGG
SPLICE FORM 1 CCTGAGCGC TTCACCTACC ACAATGTGCG CCTCTGGGAT GAGGAGTCGG
SPLICE FORM 3 CCTGAGCGC TTCACCTACC ACAATGTGCG CCTCTGGGAT GAGGAGTCGG
1251 1300
SPLICE FORM 2 CCCAGCTGCT GCCGCACTGG AAGGAGACGC ACCGCTTCAT TGAGGCTGCA
SPLICE FORM 1 CCCAGCTGCT GCCGCACTGG AAGGAGACGC ACCGCTTCAT TGAGGCTGCA
SPLICE FORM 3 CCCAGCTGCT GCCGCACTGG AAGGAGACGC ACCGCTTCAT TGAGGCTGCA
1301 1350
SPLICE FORM 2 AGAGCACAGG GCACCCACGT GCTGGTCCAC TGCAAGATGG GCGTCAGCCG
SPLICE FORM 1 AGAGCACAGG GCACCCACGT GCTGGTCCAC TGCAAGATGG GCGTCAGCCG

FIGURE 3, page 4 of 8

SPLICE FORM 3 AGAGCACAGG GCACCCACGT GCTGGTCCAC TGCAAGATGG GCGTCAGCCC

1351 1400

SPLICE FORM 2 CTCAGCGGCC ACAGTGCTGG CCTATGCCAT GAAGCAGTAC GAATGCAGCC

SPLICE FORM 1 CTCAGCGGCC ACAGTGCTGG CCTATGCCAT GAAGCAGTAC GAATGCAGCC

SPLICE FORM 3 CTCAGCGGCC ACAGTGCTGG CCTATGCCAT GAAGCAGTAC GAATGCAGCC

1401 1450

SPLICE FORM 2 TGGAGCAGGC CCTGCGCCAC GTGCAGGAGC TCCGGCCCAT CGCCCGCCCC

SPLICE FORM 1 TGGAGCAGGC CCTGCGCCAC GTGCAGGAGC TCCGGCCCAT CGCCCGCCCC

SPLICE FORM 3 TGGAGCAGGC CCTGCGCCAC GTGCAGGAGC TCCGGCCCAT CGCCCGCCCC

1451 1500

SPLICE FORM 2 AACCTGGCT TCCTGCGCCA GCTGCAGATC TACCAGGGCA TCCTGACGGC

SPLICE FORM 1 AACCTGGCT TCCTGCGCCA GCTGCAGATC TACCAGGGCA TCCTGACG..

SPLICE FORM 3 AACCTGGCT TCCTGCGCCA GCTGCAGATC TACCAGGGCA TCCTGACG..

1501 1550

SPLICE FORM 2 CAGCCGCCAG AGCCATGTCT GGGAGCAGAA AGTGGGTGGG GTCTCCCCAG

SPLICE FORM 1

SPLICE FORM 3

1551 1600

SPLICE FORM 2 AGGAGCACCC AGCCCTGAA GTCTCTACAC CATTCCTACT TCTTCCGCCA

SPLICE FORM 1GCCA

SPLICE FORM 3GCCA

1601 1650

SPLICE FORM 2 GAACCTGAGG GTGGTGGGGA GGAGAAGGTT GTAGGCATGG AAGAGAGCCA

SPLICE FORM 1 GAACCTGAGG GTGGTGGGGA GGAGAAGGTT GTAGGCATGG AAGAGAGCCA

SPLICE FORM 3 GAACCTGAGG GTGGTGGGGA GGAGAAGGTT GTAGGCATGG AAGAGAGCCA

1651 1700

SPLICE FORM 2 GGCAGCCCCG AAAGAAGAGC CTGGG..CCA CGGCCACGTA TAAACCTCCG

SPLICE FORM 1 GGCAGCCCCG AAAGAAGAGC CTGGG..CCA CGGCCACGTA TAAACCTCCG

SPLICE FORM 3 GGCAGCCCCG AAAGAAGAGC CTGGGGCCAC GGGGCACGTA TAAACCTCCG

1701 1750

SPLICE FORM 2 AGGGGTCATG AGGTCCATCA GTCTTCTGGA GCCCTCCTT. GGAGCTGGAG

SPLICE FORM 1 AGGGGTCATG AGGTCCATCA GTCTTCTGGA GCCCTCCTT. GGAGCTGGAG

SPLICE FORM 3 AGGGGTCATG AGGTCCATCA GTCTTCTGGA GCCCTCCTTG GGAGCTGGAG

1751 1800

SPLICE FORM 2 AGCACCTCAG .AGACCACTG ACATGCCAGA GGTCTTCTCT TCCCACGAGT

SPLICE FORM 1 AGCACCTCAG .AGACCACTG ACATGCCAGA GGTCTTCTCT TCCCACGAGT

SPLICE FORM 3 AGCACCTCAG TAGACCACTG ACATGCCAGA GGTCTTCTCT TCCCACGAGT

1801 1850

SPLICE FORM 2 CTTACATGA AGAGCCTCTG CAGCCCTTCC CACAGCTTGC AAGGACCAAG

SPLICE FORM 1 CTTACATGA AGAGCCTCTG CAGCCCTTCC CACAGCTTGC AAGGACCAAG

SPLICE FORM 3 CTTACATGA AGAGCCTCTG CAGCCCTTCC CACAGCTTGC AAGGACCAAG

1851 1900

SPLICE FORM 2 GGAGGCCAGC AGGTGGACAG GGGGCCTCAG CCTGCCCTGA AGTCCCGCCA

SPLICE FORM 1 GGAGGCCAGC AGGTGGACAG GGGGCCTCAG CCTGCCCTGA AGTCCCGCCA

SPLICE FORM 3 GGAGGCCAGC AGGTGGACAG GGGGCCTCAG CCTGCCCTGA AGTCCCGCCA

1901 1950

SPLICE FORM 2 GTCAGTGGTT ACCCTCCAGG GCAGTGCCGT GGTGGCCAAC CGGACCCAGG

SPLICE FORM 1 GTCAGTGGTT ACCCTCCAGG GCAGTGCCGT GGTGGCCAAC CGGACCCAGG

SPLICE FORM 3 GTCAGTGGTT ACCCTCCAGG GCAGTGCCGT GGTGGCCAAC CGGACCCAGG

1951 2000

FIGURE 3, page 5 of 8

SPLICE FORM 2 CCTTCCAGGA GCAGGAGCAG GGGCAGGGGC AGGGGCAGGG AGAGCCCTGC
 SPLICE FORM 1 CCTTCCAGGA GCAGGAGCAG GGGCAGGGGC AGGGGCAGGG AGAGCCCTGC
 SPLICE FORM 3 CCTTCCAGGA GCAGGAGCAG GGGCAGGGGC AGGGGCAGGG AGAGCCCTGC

2001 2050
 SPLICE FORM 2 ATTTCCCTCTA CGCCCAGGTT CCGGAAGGTG GTGAGACAGG CCAGCGTGCA
 SPLICE FORM 1 ATTTCCCTCTA CGCCCAGGTT CCGGAAGGTG GTGAGACAGG CCAGCGTGCA
 SPLICE FORM 3 ATTTCCCTCTA CGCCCAGGTT CCGGAAGGTG GTGAGACAGG CCAGCGTGCA

2051 2100
 SPLICE FORM 2 TGACAGTGGA GAGGAGGGCG AGGCCTGAGC CCTCACACAT GCCCAGGCTC
 SPLICE FORM 1 TGACAGTGGA GAGGAGGGCG AGGCCTGAGC CCTCACACAT GCCCAGGCTC
 SPLICE FORM 3 TGACAGTGGA GAGGAGGGCG AGGCCTGAGC CCTCACACAT GCCCAGGCTC

2101 2150
 SPLICE FORM 2 CCCTGACACT GAAGAGGATC CACAACCTCCT TGGAGAAACA CCCTCACGTC
 SPLICE FORM 1 CCCTGACACT GAAGAGGATC CACAACCTCCT TGGAGAAACA CCCTCACGTC
 SPLICE FORM 3 CCCTGACACT GAAGAGGATC CACAACCTCCT TGGAGAAACA CCCTCACGTC

2151 2200
 SPLICE FORM 2 TGTTGCCGCA CACATTCCCTC TCAGCTCCGC CCCATACCCG TCACTACAGC
 SPLICE FORM 1 TGTTGCCGCA CACATTCCCTC TCAGCTCCGC CCCATACCCG TCACTACAGC
 SPLICE FORM 3 TGTTGCCGCA CACATTCCCTC TCAGCTCCGC CCCATACCCG TCACTACAGC

2201 2250
 SPLICE FORM 2 CTCACCTCCC ACCCCTGTCA CTACGGCCTC ACCTCCCACC CCTGTCACTA
 SPLICE FORM 1 CTCACCTCCC ACCCCTGTCA CTACGGCCTC ACCTCCCACC CCTGTCACTA
 SPLICE FORM 3 CTCACCTCCC ACCCCTGTCA CTACGGCCTC ACCTCCCACC CCTGTCACTA

2251 2300
 SPLICE FORM 2 CAGCCTCACC TCCTACAGCC TTAAGTCCCA GGCCCATGTC TGCCTGTCCA
 SPLICE FORM 1 CAGCCTCACC TCCTACAGCC TTAAGTCCCA GGCCCATGTC TGCCTGTCCA
 SPLICE FORM 3 CAGCCTCACC TCCTACAGCC TTAAGTCCCA GGCCCATGTC TGCCTGTCCA

2301 2350
 SPLICE FORM 2 AGGGCTCAAG ACTTTCTAAC TGGGATGTGG TAGAGGGACT GAAGGTACCT
 SPLICE FORM 1 AGGGCTCAAG ACTTTCTAAC TGGGATGTGG TAGAGGGACT GAAGGTACCT
 SPLICE FORM 3 AGGGCTCAAG ACTTTCTAAC TGGGATGTGG TAGAGGGACT GAAGGTACCT

2351 2400
 SPLICE FORM 2 TTGGGGGGCAA CAGCACCCCTA GTTTCATTCT CAACTCTAGC CCTGCACACT
 SPLICE FORM 1 TTGGGGGGCAA CAGCACCCCTA GTTTCATTCT CAACTCTAGC CCTGCACACT
 SPLICE FORM 3 TTGGGGGGCAA CAGCACCCCTA GTTTCATTCT CAACTCTAGC CCTGCACACT

2401 2450
 SPLICE FORM 2 CACCTGTGGC ACGGAATGAA AACAGAGCTT CCCGTGCAAA AAGGGTCACG
 SPLICE FORM 1 CACCTGTGGC ACGGAATGAA AACAGAGCTT CCCGTGCAAA AAGGGTCACG
 SPLICE FORM 3 CACCTGTGGC ACGGAATGAA AACAGAGCTT CCCGTGCAAA AAGGGTCACG

2451 2500
 SPLICE FORM 2 CCTCCCACCC CCGCCCCCTC CCTGCACCTC CTGTCCTCTC CCAGTTCATT
 SPLICE FORM 1 CCTCCCACCC CCGCCCCCTC CCTGCACCTC CTGTCCTCTC CCAGTTCATT
 SPLICE FORM 3 CCTCCCACCC CCGCCCCCTC CCTGCACCTC CTGTCCTCTC CCAGTTCATT

2501 2550
 SPLICE FORM 2 CCTGGAACCA GCCAGGCCAG GCAACCAGTG GCCCCCAAAG GCAGGCAGGA
 SPLICE FORM 1 CCTGGAACCA GCCAGGCCAG GCAACCAGTG GCCCCCAAAG GCAGGCAGGA
 SPLICE FORM 3 CCTGGAACCA GCCAGGCCAG GCAACCAGTG GCCCCCAAAG GCAGGCAGGA

2551 2600
 SPLICE FORM 2 TCCTCAGGCC CCAGCCGCGG GAGGCTGGAA GGGCTGGCAG ATCGCTTCCC
 SPLICE FORM 1 TCCTCAGGCC CCAGCCGCGG GAGGCTGGAA GGGCTGGCAG ATCGCTTCCC
 SPLICE FORM 3 TCCTCAGGCC CCAGCCGCGG GAGGCTGGAA GGGCTGGCAG ATCGCTTCCC

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SPLICE FORM 2 ELRLGLPLQQ YRDFIDNQML LLVAQRDRAS RIFPHLYLGS EWNAANLEEL
SPLICE FORM 1 ELRLGLPLQQ YRDFIDNQML LLVAQRDRAS RIFPHLYLGS EWNAANLEEL
SPLICE FORM 3 ELRLGLPLQQ YRDFIDNQML LLVAQRDRAS RIFPHLYLGS EWNAANLEEL

351 400
SPLICE FORM 2 QRNRVTHILN MAREIDNFYP ERFTYHNVRL WDEESAQLLP HWKETHRFIE
SPLICE FORM 1 QRNRVTHILN MAREIDNFYP ERFTYHNVRL WDEESAQLLP HWKETHRFIE
SPLICE FORM 3 QRNRVTHILN MAREIDNFYP ERFTYHNVRL WDEESAQLLP HWKETHRFIE

401 450
SPLICE FORM 2 AARAQGTHVL VHCKMGVSRS AATVLAYAMK QYECSEALQAL RHVQELRPIA
SPLICE FORM 1 AARAQGTHVL VHCKMGVSRS AATVLAYAMK QYECSEALQAL RHVQELRPIA
SPLICE FORM 3 AARAQGTHVL VHCKMGVSRS AATVLAYAMK QYECSEALQAL RHVQELRPIA

451 500
SPLICE FORM 2 RPNPGFLRQL QIYQGILTAS RQSHVWEQKV GGVSPPEHPA PEVSTPFLL
SPLICE FORM 1 RPNPGFLRQL QIYQGILTAR T~~~~~ ~~~~~~ ~~~~~~
SPLICE FORM 3 RPNPGFLRQL QIYQGILTAR T~~~~~ ~~~~~~ ~~~~~~

501 550
SPLICE FORM 2 PPEPEGGEE KVVGMEESEA APKEEPGPRP RINLRGVMRS ISLLEPSLEL
SPLICE FORM 1 ~~~~~~ ~~~~~~ ~~~~~~ ~~~~~~ ~~~~~~
SPLICE FORM 3 ~~~~~~ ~~~~~~ ~~~~~~ ~~~~~~ ~~~~~~

551 600
SPLICE FORM 2 ESTSETSDMP EVFSSHESSH EEPLQFPFQL ARTKGGQQVD RGPQPAKLSR
SPLICE FORM 1 ~~~~~~ ~~~~~~ ~~~~~~ ~~~~~~ ~~~~~~
SPLICE FORM 3 ~~~~~~ ~~~~~~ ~~~~~~ ~~~~~~ ~~~~~~

601 650
SPLICE FORM 2 QSVVTLQGS VVANRTQAFQ EQEQGGQGGQ GEPCISSTPR FRKVVRQASV
SPLICE FORM 1 ~~~~~~ ~~~~~~ ~~~~~~ ~~~~~~ ~~~~~~
SPLICE FORM 3 ~~~~~~ ~~~~~~ ~~~~~~ ~~~~~~ ~~~~~~

651
SPLICE FORM 2 HDSGEEGEA
SPLICE FORM 1 ~~~~~~
SPLICE FORM 3 ~~~~~~

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